



85189-49001rev.txt
SEQUENCE LISTING

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Shav-Tal, Yaron

<120> T CELL RECEPTOR VARIANTS EXPRESSED IN MESENCHYMAL CELLS AND USES THEREOF

<130> 85189-4900

<140> 10/642,642

<141> 2003-08-19

<150> PCT/IL 02/00130

<151> 2002-02-20

<150> 141539

<151> 2001-02-20

<160> 86

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<210> 1

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<212> PRT

<213> Mus musculus

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Arg Gly Arg Ile Leu Gly Ser Pro Phe Leu
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Met Gly Glu Tyr Leu Ala Glu Pro Arg Gly Phe Val Cys Gly Val Glu
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Pro Leu Cys

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Met Glu Ala Gly Trp Glu Val Gln His Trp Val Ser Asp Met Glu Cys
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Leu Thr Val

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Met Thr Val
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Met Cys Gly Ser Glu Glu Val Phe Val Val Glu Ser Ala
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Met Ala Cys Tyr Gln Met Tyr Phe Thr Gly Arg Lys Val Asp Glu Pro
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Ser Glu Leu Gly Ser Gly Leu Glu Leu Ser Tyr Phe His Thr Gly Gly
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Ser Ser Gln Ala Val Gly Leu Phe Ile Glu Asn Met Ile Ser Thr Ser
 35 40 45

His Gly His Phe Gln Glu Met Gln Phe Ser Ile Trp Ser Phe Thr Val
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Leu Gln Ile Ser Ala Pro Gly Ser His Leu Val Pro Glu Thr Glu Arg
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Ala Glu Gly Pro Gly Val Phe Val Glu His Asp Ile
 85 90

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Met Tyr Phe Thr Gly Arg Lys Val Asp Glu Pro Ser Glu Leu Gly Ser
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Gly Leu Glu Leu Ser Tyr Phe His Thr Gly Gly Ser Ser Gln Ala Val
 20 25 30

Gly Leu Phe Ile Glu Asn Met Ile Ser Thr Ser His Gly His Phe Gln
 35 40 45

Glu Met Gln Phe Ser Ile Trp Ser Phe Thr Val Leu Gln Ile Ser Ala
 50 55 60

Pro Gly Ser His Leu Val Pro Glu Thr Glu Arg Ala Glu Gly Pro Gly
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Val Phe Val Glu His Asp Ile
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Met Ile Ser Thr Ser His Gly His Phe Gln Glu Met Gln Phe Ser Ile
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Trp Ser Phe Thr Val Leu Gln Ile Ser Ala Pro Gly Ser His Leu Val
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Pro Glu Thr Glu Arg Ala Glu Gly Pro Gly Val Phe Val Glu His Asp
 35 40 45

Ile

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Met Gln Phe Ser Ile Trp Ser Phe Thr Val Leu Gln Ile Ser Ala Pro
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Gly Ser His Leu Val Pro Glu Thr Glu Arg Ala Glu Gly Pro Gly Val
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Phe Val Glu His Asp Ile
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Met Trp Trp Gly Leu Ile Leu Ser Ala Ser Val Lys Phe Leu Gln Arg
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Lys Glu Ile Leu Cys
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Met Val Gly Ala Asp Leu Cys Lys Gly Gly Trp His Cys Val
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Met Arg Glu Pro Val Lys Asn Leu Gln Gly Leu Val Ser
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Met Glu Val Tyr Glu Leu Arg Val Thr Leu Met Glu Thr Gly Arg Glu
 1 5 10 15

Arg Ser His Phe Val Lys Thr Ser Leu
 20 25

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Met Glu Thr Gly Arg Glu Arg Ser His Phe Val Lys Thr Ser Leu
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 <212> PRT
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Met Gly Leu Ser Ala Val Gly Arg Thr Arg Ala Glu Ser Gly Thr Ala
 1 5 10 15

Glu Arg Ala Ala Pro Val Phe Val Leu Gly Leu Gln Ala Val
 20 25 30

<210> 18
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Met Leu Leu Trp Asp Pro Ser Gly Phe Gln Gln Ile Ser Ile Lys Lys
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Val Ile Ser Lys Thr Leu Pro Thr
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<210> 19
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Met Leu Pro Asn Thr Met Gly Gln Leu Val Glu Gly Gly His Met Lys
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Gln Val Leu Ser Lys Ala Val Leu Thr Val
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<213> Homo sapiens

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Met Gly Gln Leu Val Glu Gly Gly His Met Lys Gln Val Leu Ser Lys
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Ala Val Leu Thr Val
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Met Lys Gln Val Leu Ser Lys Ala Val Leu Thr Val
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Met Ser Glu Cys
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Met Ala His Phe Val Ala Val Gln Ile Thr Val
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Met Gly Ile Cys Tyr Ser
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Met Lys Arg Ala Gly Glu Gly Lys Ser Phe Cys Lys Gly Arg His Tyr
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Ser Val

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1 5 10 15Arg Gln His Ser Ala
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<211> 37

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<213> Homo sapiens

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1 5 10 15Val Phe Ile Gln Gln Leu Ser Ser Leu Gly Lys Pro Phe Cys Arg Gly
20 25 30Val Cys His Ser Val
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<211> 11

<212> PRT

<213> Homo sapiens

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Met Gly Phe Ser Lys Gly Arg Lys Cys Cys Gly
Page 7

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5

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Met Lys Lys Ile Trp Leu Ser Arg Lys Val Phe Leu Tyr Trp Ala Glu
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Thr Leu

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Met Gly Lys Val His Val Met Pro Leu Leu Phe Met Glu Ser Lys Ala
 1 5 10 15

Ala Ser Ile Asn Gly Asn Ile Met Leu Val Tyr Val Glu Thr His Asn
 20 25 30

Thr Val

<210> 31
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<400> 31

Met Pro Leu Leu Phe Met Glu Ser Lys Ala Ala Ser Ile Asn Gly Asn
 1 5 10 15

Ile Met Leu Val Tyr Val Glu Thr His Asn Thr Val
 20 25

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<400> 32

Met Glu Ser Lys Ala Ala Ser Ile Asn Gly Asn Ile Met Leu Val Tyr
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Val Glu Thr His Asn Thr Val
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Met Leu Val Tyr Val Glu Thr His Asn Thr Val
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Met Glu Glu Gly Ser Phe Ile Tyr Thr Ile Lys Gly Pro Trp Met Thr
1 5 10 15

His Ser Leu Cys Asp Cys Cys Val Ile Gly Phe Gln Thr Leu Ala Leu
20 25 30

Ile Gly Ile Ile Gly Glu Gly Thr Trp Trp Leu Leu Gln Gly Val Phe
35 40 45

Cys Leu Gly Arg Thr His Cys
50 55

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Met Thr His Ser Leu Cys Asp Cys Cys Val Ile Gly Phe Gln Thr Leu
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Ala Leu Ile Gly Ile Ile Gly Glu Gly Thr Trp Trp Leu Leu Gln Gly
20 25 30

Val Phe Cys Leu Gly Arg Thr His Cys
35 40

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85189-49001rev.txt

Met Glu Ser Gln Ala Thr Gly Phe Cys Tyr Glu Ala Ser His Ser Val
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Leu Ala Glu Pro Arg Gly Phe Val Cys Gly Val Glu
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<223> intron 5 prime to J beta 2.6

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<223> C beta 2 domain

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gaaatgtgac tccaccaag gtctccttgt ttgagccatc aaaagcagag attgcaaaca 180
aacaaaaggc taccctcgtg tgcttgGCCa ggggcttctt ccctgaccac gtggagctga 240
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cttcaccctg gccatagatt ttctgcacc ttctctaatt cctgttccta agaactgtc 720
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Met Gly Glu Tyr Leu Ala Glu Pro Arg Gly Phe Val Cys Gly Val Glu
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Pro Leu Cys Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu Thr
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Val Leu Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe
 35 40 45

Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu Val
 50 55 60

Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp
 65 70 75 80

Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Ala
 85 90 95

Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val
 100 105 110

Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln Val
 115 120 125

Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser Pro
 130 135 140

Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala Asp
 145 150 155 160

Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu Ser Ala Thr
 165 170 175

Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu
 180 185 190

Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys Asn Ser
 195 200 205

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Lys Gly Ser Arg Glu Val Glu Pro Pro Phe Ser Pro Tyr His Val Asn
 1 5 10 15

His Gln Gln Ser Ile Arg Thr Cys Met Gly Asn Tyr Glu Leu Ile Lys
 20 25 30

Lys His Val Glu Lys Thr Leu Cys Gly Lys Glu Val Thr Ser Pro Phe
 35 40 45

Ser Leu Glu Ala Thr Trp Thr Pro Thr Gly Ser Leu Gln Ile Ser Asn
 50 55 60

Ser Leu Cys Gln Thr Leu Ser Glu Met Asp Ile Arg Ser Gln Ala Lys
 65 70 75 80

Ser Gly Ile Ser Ser Ser Ile Asp Arg Pro His Ala Arg Ser Arg Leu
 85 90 95

Pro Tyr Gln Phe Trp Arg Met Glu Asn Val Ser Asn Pro Gly Ser Cys
 100 105 110

Ile Glu Glu Gly Glu Glu Arg Gly Arg Ile Leu Gly Ser Pro Phe Leu
 115 120 125

Leu

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 <223> J beta 2.6 sequence

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Glu Leu Leu Gly Asn Cys Ser Gly Glu Phe Trp Gly Phe Trp Arg Leu
 1 5 10 15

Tyr Pro Glu Phe Pro Ser Arg Ala Leu Glu Arg Glu Ala Glu Gln Gly
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85189-49001rev.txt

Asp Phe Pro Met Gly Glu Tyr Leu Ala Glu Pro Arg Gly Phe Val Cys
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Gly Val Glu Pro Leu Cys
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<400> 42

Val Ser Lys Lys Lys Lys Lys Lys Lys Ser Val Thr Ile Leu Asn Ser
 1 5 10 15

Glu Pro Ala Glu Gly Ala Ile Asn Ser Ser Leu Leu Gly Ser Leu Asp
 20 25 30

Pro Gly Asn Val Leu Glu His Cys Thr Gly Leu Leu Pro Ser Pro Lys
 35 40 45

Asp Asp Pro Cys Gln Asp Arg Ser Ser Phe Leu Trp Gly Gly Gly Gln
 50 55 60

Trp Ile Phe Ala Val Ile Val Phe Cys Leu Ala His Ser Pro Arg Leu
 65 70 75 80

Trp Pro Glu Thr Ser Pro Gln Ser Thr Thr Gln Glu Gln Arg Val Lys
 85 90 95

Gly Leu Asn Gly Glu Arg Asp Ile Gly His Val Arg Thr Arg Arg Asn
 100 105 110

Phe Thr Gln Lys Lys Asn Cys His Leu Gly Arg Cys Ser Val Ser Met
 115 120 125

Ala Glu Val Thr Pro Pro Pro Cys Pro Arg Leu Val Ser Gln Leu Arg
 130 135 140

His Gly His Gln Lys Gly Gly Phe Leu Ser Ser Leu Lys Thr Asn Leu
 145 150 155 160

Ala Glu Ser His Leu Pro Ser Ser Pro Asn Glu Pro Val Val Ser Val
 Page 13

165

170

175

Asp Ala Leu Gly Ser Val Arg Arg Val Phe Ala Val Ala Glu Gly Ser
 180 185 190

Arg Leu Thr Arg Arg Ala Arg Trp Gly Arg Thr Tyr Arg Gly Trp Thr
 195 200 205

Glu Ala Ser Pro Cys Leu His Ser Ser Cys Ala Ala Ser Ser Cys Gly
 210 215 220

Phe Thr Gly Gly Arg Gly Gly Trp Gly Arg Gly Ala Ile Pro Lys Ala
 225 230 235 240

Val Ala Cys Phe Gly Ile Cys Ser Gly Leu Leu Cys Leu Pro Pro Trp
 245 250 255

Glu Arg Thr His Leu Ala Ser Arg Arg Leu Asp Val Ala Gly Gln Glu
 260 265 270

Asp Thr Gly Val Gly Gly Asn Ser Phe Arg Gly Glu Gly Glu Arg Gly
 275 280 285

Gly Arg Thr Val Val Glu Gly Val Thr Gly Gly Ser Met Ser Arg Met
 290 295 300

Ser Glu Val Lys Phe Lys Lys Leu Glu Ile Lys Asn Lys Lys Gln Gly
 305 310 315 320

Arg Gly Leu Gln Lys Val Tyr Arg Ala Gly Thr Val Asp Phe Val Met
 325 330 335

Ala Trp His Thr
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 <222> (1)..(253)
 <223> J alpha TA46 sequence

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Val Phe Leu Pro Gly Arg Trp Glu Pro Lys Glu Val Asp Arg Asp Ile
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85189-49001rev.txt

Ser Asn Pro Pro Cys Lys Pro Leu Val Leu Pro Thr Val Asp Thr Val
20 25 30

Thr Ile Arg Thr Leu Ser His Ile Asp Glu Gly Ser Asp Val Val His
35 40 45

Thr Glu Asp Ser Arg Asp Leu Ser Leu Val Thr Val Ser Asp Cys Met
50 55 60

Pro Ile Val Val His Ser Arg Val Gln Gln Thr Lys Asp Arg Asp Ile
65 70 75 80

Lys Ile Arg Trp Thr Leu Ser Pro His Leu Cys Asn Gln Met Ile Phe
85 90 95

Thr Gly Ser Leu Ala Asn Gly Cys Val Ala Ser Leu Thr Ile Ser Pro
100 105 110

Leu Leu Ser Pro Trp Leu Ser Phe Gly Ser Leu Ser Leu Thr Asn Leu
115 120 125

Lys Ser Ile Tyr Ile Ile Arg Phe Leu Gly Cys Ile Thr His Lys Lys
130 135 140

Met Thr Ser Arg His Ile Asn Ile Asn Pro Glu Glu Arg Gly Gln Arg
145 150 155 160

Ala Leu Ser Gln Thr Cys Ser Glu Leu Asn Leu Thr Thr Pro Cys Phe
165 170 175

Asn Gln Leu Ala Ser Ala Tyr Asp Gln Leu Arg Gln Arg Ala Thr Asp
180 185 190

Arg Lys Trp Ser Ser Arg His His Leu Thr Arg Ala Leu Pro His Gln
195 200 205

Arg Tyr Phe Arg Val Gln Glu Ser Phe Pro Gln Ala Gly Trp Leu Glu
210 215 220

Arg Gly His Gly Ser Ala Leu Arg Gln Ala Met Glu Ala Gly Trp Glu
225 230 235 240

Val Gln His Trp Val Ser Asp Met Glu Cys Leu Thr Val
245 250

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<212> PRT
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<220>
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 <222> (1)..(310)
 <223> J alpha New05 sequence

<400> 44

Val Lys Asp Gly Tyr Pro Lys Thr Lys Val Cys Gly Phe Ala Val Leu
 1 5 10 15

Cys Ser Phe Gly Gly Cys Met Ser Leu Pro Pro Arg Ser Leu Cys Ile
 20 25 30

Thr Leu Met Gly Leu Cys Leu Met Lys Ser Gly His Ser Lys Asp Leu
 35 40 45

Asp Glu Glu Val Ile Ile Ile Thr Ala Phe Phe His Tyr Leu Arg Ile
 50 55 60

Arg Ser Ala Arg Phe Ile Asn Val Arg Leu Met Phe Val Leu Arg Tyr
 65 70 75 80

Lys Pro Asn Asn Ser Lys Ile Arg Leu Ser Ser Val Thr Thr His Ile
 85 90 95

His Thr His Ser His Thr His Ile Leu Thr His Trp His Asn His Thr
 100 105 110

His Thr His Thr Leu Ser Gln Ser His Thr His Thr His Ser His Thr
 115 120 125

Ser Thr Ile Thr His Thr Leu Thr Gln Pro His Thr His Ser Leu Ser
 130 135 140

Leu Ser Leu Ser Leu Ser Leu Ser Leu Ser Leu Ser Leu Ser
 145 150 155 160

Leu Pro Arg Gln Cys Asn Cys Ile Trp Phe Pro Ser Arg Asn Gly Cys
 165 170 175

Cys Val Cys Leu Thr Asp Met Gln Ser Tyr Gln Leu Val Ser Trp Leu
 180 185 190

Gly Phe Cys Tyr Cys Phe Ser Val Lys Thr Leu Pro Val Lys Glu Ala
 195 200 205

Trp Cys Tyr Gln Pro Ser Cys His Tyr Ser Asn His Ile Tyr Thr Pro
 210 215 220

Phe Tyr Tyr Phe Ile Ser Leu Lys Leu Ala Gln Leu Ile Arg Ile Gln
 225 230 235 240

Cys Trp Gly Asn Lys Thr Ser Gly Phe Ser Ser Ser Glu Leu His Ser
 245 250 255

Gln Leu Leu Val Leu Arg Gly Cys Ser Lys Pro Ser Gln Thr Leu Gly
 260 265 270

Thr Lys Ala Ala Arg Arg Lys Ala Ser Thr Arg Gly Glu Asp Asp Val
 275 280 285

Ala Phe Leu Gly Leu Pro Leu Gly Pro Ser Cys Leu Leu Val Ile Val
 290 295 300

Arg Pro Gln Met Thr Val
 305 310

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Trp Val Arg Phe His Val Thr Ala Val Ala Leu Cys Ser Phe Thr Ser
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Leu Leu His Leu Phe Leu Glu Thr Leu Gly Phe Arg Leu Ser Phe Leu
 20 25 30

Phe Lys Lys Gln Ser Leu Ser Lys Gln Asp Leu Leu Cys Leu Leu Ser
 35 40 45

Phe His Ile Val Thr Lys Ala Gly Arg Ile Cys Ser Lys Leu Gly Leu
 50 55 60

Arg Leu Leu Ala Lys Val Glu Trp Met Val Leu Val Tyr Arg Lys Glu
 65 70 75 80

Arg Phe Val Leu Leu Phe Phe Pro Tyr Ser Lys Val Lys Ala Thr Thr
 85 90 95

Val Ala Ser Lys Val Leu Gln Ala Trp Ser Val Leu Gln Gly Glu Thr
 100 105 110
 Trp Gly Asn Trp Leu Thr Phe His Gly Lys Thr Gly Met Leu Phe Val
 115 120 125
 Val Gly Leu Leu Leu Leu Leu Leu Ser Ser Leu Ser Leu Ser Leu Lys
 130 135 140
 Glu Thr Tyr Asn Thr Phe Leu Ser Gly Phe Glu Leu Gly Ile Gln Met
 145 150 155 160
 Cys Ile Thr Cys Ser Trp Gln Gly Ser Arg Ala Val Val Leu Asn Leu
 165 170 175
 Pro Asn Val Val Ala Pro Ser Pro Pro Lys Thr Ile Lys Leu Phe Cys
 180 185 190
 Cys Tyr Phe Ile Ala Val Thr Leu Leu Leu Leu Ile Gly Met Ile Ser
 195 200 205
 Tyr Met Gln Leu Ile Tyr Ala Thr Pro Val Lys Gly Ser Leu Asn Pro
 210 215 220
 Gln Arg Arg Ser Ala Leu Gln Asp Glu Ser Arg Cys Cys Arg Gly Arg
 225 230 235 240
 Trp Ser Thr Val Ser Asn Val Arg Gly Ala Ile Glu Leu Gly Arg Asn
 245 250 255
 Thr Met Pro Thr Phe Glu Glu Lys Lys Asn Ser Ser Leu Gly Leu Glu
 260 265 270
 Gln Asp Pro Leu Phe Leu Val Ser Pro Leu Pro Leu Glu Lys Lys Pro
 275 280 285
 Phe Ile Cys Asn Gly Leu Ser Arg Leu Met Ser Phe Met Arg Phe His
 290 295 300
 Val Leu Thr Asp Ser Leu Gly Arg Arg Ser Leu Leu Pro Leu Gln Val
 305 310 315 320
 Val Phe Asp Val Gly Asn Val Asn Cys Thr Ala Lys Ile Arg Arg Ala
 325 330 335
 Gly Ile Asn Ser Gln Pro Leu Leu Met Leu Ser Leu Asn Arg Asn Gln

340

345

350

Ile Arg Met Leu Ser Ser Val Cys Val His Thr Pro Pro Arg Ala Ser
 355 360 365

Phe Asp Cys Gln Leu Ile Gln Ile Phe Arg His Leu Ser Glu Gln Thr
 370 375 380

Ser Leu Gly Ser Leu Cys Leu Asn Leu Ser Arg Tyr Leu His Asn Cys
 385 390 395 400

Gln Ile Cys Phe Thr Leu Cys Cys Ile Asp Ser Ala Lys Gln Met Arg
 405 410 415

Leu Cys Phe Pro Arg Ser Phe Ser Pro Arg Arg Ser Ser Leu Pro Pro
 420 425 430

Ser Lys His Leu Phe Thr Gln Arg Glu Asp Val Gln Arg Val Thr Leu
 435 440 445

Ile Ala Ala Ala Ser Leu His Leu Tyr Asp Ser Leu Pro Trp Lys Arg
 450 455 460

Leu Lys His Phe Ile Arg Leu Ile Ser Thr Asp Gln Pro Asn Glu Glu
 465 470 475 480

Arg Asn Arg Phe Ala Ser Phe Leu Trp Leu Gln Phe Gln Ala Thr His
 485 490 495

Leu Glu His Leu Val Arg His Leu Arg Asn Thr Gly Ala Arg Arg Glu
 500 505 510

Val Val Ser Leu Cys Gly Leu Val Phe Leu Ser Cys Thr Glu Asn Phe
 515 520 525

Thr Gln Glu Glu Glu Ser Lys Val Glu Asn Gln Pro Gly Ile His Met
 530 535 540

Tyr Thr Lys Gln Ser Ala Ser Ala Leu Ser Gly Ser Thr Val Trp Phe
 545 550 555 560

Pro His Ser Pro Thr Pro Ala Pro Phe Ile Ser Asn Thr Tyr Ile Ile
 565 570 575

Leu Phe Ser Phe Ser Phe Glu Phe Leu Ser Ala Met Pro Ser His Asn
 580 585 590

Pro Ser Thr Tyr His Cys Leu Ser Asn Pro Arg Met Asp Gly Ser Gly
 595 600 605

Thr Gly Arg Val Leu Phe Ser Gly Pro Ser Ala Glu Pro Leu Lys Lys
 610 615 620

Cys Arg Leu Tyr Pro Ser Ser Val Ala Thr Arg Arg Leu Gly Arg Gly
 625 630 635 640

Gln Asp Glu Glu Lys Pro Gln Glu Ser Gly Thr Ala Ser Leu Trp Tyr
 645 650 655

Ile Arg Leu Asn Leu Leu Ser Gly Leu Lys Cys Phe Ser Phe His Leu
 660 665 670

Glu Pro Met Cys Gly Ser Glu Glu Val Phe Val Val Glu Ser Ala Thr
 675 680 685

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 <223> J alpha New06 sequence

<400> 46

Lys Cys Val Phe Ser Cys Ser Leu Gly Leu Glu Gln Tyr Cys Ser Leu
 1 5 10 15

His Pro Gln Ile Phe Ser Arg Arg Ile Gln Cys Leu Ala Leu Gln Thr
 20 25 30

Leu Pro Val Pro Leu Lys Gly Ser Tyr Ser Phe Phe Lys His Arg Arg
 35 40 45

Ile Pro Phe Asn Val Ala Asn Cys Gly Gly Asp Thr Ala Gln Gly Pro
 50 55 60

Asn Leu Cys Ser Ser Leu Leu Gly Gln Leu Cys Leu Leu Ser His Arg
 65 70 75 80

Thr Ser Glu Ser Gly Gly Leu Phe Pro Ser Leu Ala Phe Pro Val Asp
 85 90 95

Glu Val Val Leu Ser Thr Asn Phe Ile Val Lys Asp Thr His Asp Arg
 100 105 110

Gln Leu Leu Pro Tyr Phe Ser Leu Asn Lys Phe Phe Leu Cys Leu Gln
 115 120 125

His Ile Ser Ala Asn Glu Phe Leu Val Ile Gln Ile Asn Ser Ser Val
 130 135 140

Thr Thr Val Ala Ser Tyr Pro Ile Ile Gln Asn Ser Leu Thr His His
 145 150 155 160

Ser Ala Ala Ala His Cys Ala Ser Ser Asn Pro Asp Leu His Ala Ser
 165 170 175

Ser Asn Lys Ala Lys Arg Met Ala Cys Tyr Gln Met Tyr Phe Thr Gly
 180 185 190

Arg Lys Val Asp Glu Pro Ser Glu Leu Gly Ser Gly Leu Glu Leu Ser
 195 200 205

Tyr Phe His Thr Gly Gly Ser Ser Gln Ala Val Gly Leu Phe Ile Glu
 210 215 220

Asn Met Ile Ser Thr Ser His Gly His Phe Gln Glu Met Gln Phe Ser
 225 230 235 240

Ile Trp Ser Phe Thr Val Leu Gln Ile Ser Ala Pro Gly Ser His Leu
 245 250 255

Val Pro Glu Thr Glu Arg Ala Glu Gly Pro Gly Val Phe Val Glu His
 260 265 270

Asp Ile Thr
 275

<210> 47
 <211> 556
 <212> PRT
 <213> Mus musculus

<220>
 <221> misc_feature
 <222> (1)..(556)
 <223> J alpha New08 sequence

<400> 47

Val Met Phe His Phe Leu Met Phe Asn Ser Leu Pro Leu Ser Arg Cys
 1 5 10 15

Ser Glu Cys Arg Val Gly Lys Leu His Met Leu Gly His Gly Gly Gln
 20 25 30

His Ser Cys Thr Gly Tyr Ser Thr Ala Gln Pro Asp Thr Thr Ser Pro
 35 40 45

Thr Thr Gly Glu Thr Ala Pro Thr Leu Pro Pro Asp Thr Lys Ile Phe
 50 55 60

Leu Ile Val Tyr Leu Ile Arg Ala Lys Gly Lys Ile Lys Lys Leu Cys
 65 70 75 80

Pro Glu Ser Ile Leu Lys Ser Pro Arg Pro Ser Pro Pro Tyr Pro His
 85 90 95

Ser Pro Ala Asp Cys Lys Phe Asn Val Ile Phe Gly Ser Tyr Lys Gly
 100 105 110

Phe Leu Cys Leu Met Thr Pro Thr Val Ser Leu Pro Ser Phe Ile Lys
 115 120 125

Gly Leu Leu Phe Cys Val Trp Pro Leu Leu Ala Ser Trp Phe Cys Pro
 130 135 140

His Ala Pro Leu Cys Leu Phe Gln Gly Trp Ala Gly Asp Asn Ser Phe
 145 150 155 160

Lys Ser His Phe Asp Val Thr Asp Asn Arg Asp Lys Val Leu Ala Lys
 165 170 175

Cys Asn Thr Ala His Gly Val Phe Ser Arg His Thr Thr Ser Gln Leu
 180 185 190

Phe Ser Ser Val Gln Lys His Gly His Ser Tyr Leu Met Ser Ala Ile
 195 200 205

Tyr Ser Asp Thr Ala Lys Cys Ser Phe Lys Ala Gly Thr Arg Asp Phe
 210 215 220

Leu Trp Asp Leu Phe Leu Arg Leu Thr Met Gly Trp Ala Phe Ser Gly
 225 230 235 240

Ser Ser Glu Met Pro Ser Trp Ile Pro Ala Leu Pro Met Glu Ile Leu
 245 250 255

Trp Ser Gly Thr Ala Lys Pro Asp Met Phe Leu Leu Tyr Arg Leu Leu
 260 265 270

85189-49001rev.txt

Gln Gly Leu Glu Ile Arg Thr Leu Arg Glu Asn Lys Ser Phe Gly Met
 275 280 285
 Gly Arg Leu Leu Asp Gly Ser Ile Arg Lys Arg Asn Asp Gln Glu Glu
 290 295 300
 Arg Pro Lys Lys Asn Thr Gly Gln Ala Leu Gly Trp Gly Gly Val Gly
 305 310 315 320
 Met Ser Arg Lys Met Val Thr Val Gly Ile Gln Glu Ala Gly Ser Leu
 325 330 335
 Ser Glu Gly Lys Gln Gly Phe Leu Leu Lys Val Pro Ser Gln Leu Ser
 340 345 350
 Asn Leu Asn Gln Gln Gly His Leu Pro Phe Pro Ser Asp Phe Pro Val
 355 360 365
 His Val Gly Met Pro Leu Pro Pro Thr Met Val Cys Glu Val Gly Arg
 370 375 380
 Gly Ile Asp Gln Glu Tyr Val His Ser Gly Pro Leu Phe Lys His Glu
 385 390 395 400
 Thr Pro Glu Ser Val Arg Gly Ala Lys Ser Leu Gly Pro Arg Arg Glu
 405 410 415
 Met Gln Gln Ser Asn Ser Ser Gln Gln Val Trp Arg Ser Thr Glu Gln
 420 425 430
 Asp Pro Val Leu Ala Leu Cys Leu Thr Pro Leu Ala Ser Pro Asp His
 435 440 445
 Thr Ala His Pro Ser Ser Phe Ser Pro Gln Glu Ser Lys Val Leu Asp
 450 455 460
 Arg Glu Pro Glu Ile Pro Pro Gly Gln Val Gln Lys Gly Trp Ser Gly
 465 470 475 480
 Ala Gln Gly Trp Phe Leu Lys Thr Leu Trp Ile Ser Ile Phe Leu Ile
 485 490 495
 Tyr Asn Lys Phe Leu Ser Val Ile Arg Lys Met Phe Leu Leu Thr Ile
 500 505 510
 Pro Val Lys Gly Lys Asp Asn Ile Tyr Arg Gly Pro Leu Leu Arg Cys
 515 520 525

Gln Phe Pro Pro Trp Ala Ser Met Trp Trp Gly Leu Ile Leu Ser Ala
 530 535 540

Ser Val Lys Phe Leu Gln Arg Lys Glu Ile Leu Cys
 545 550 555

<210> 48
 <211> 604
 <212> PRT
 <213> Mus musculus

<220>
 <221> misc_feature
 <222> (1)..(604)
 <223> J alpha LB2A sequence

<400> 48

Val Ile Val Thr His Pro Leu Cys Ile Pro Pro Thr Arg Ser Ile Phe
 1 5 10 15

Ala Leu Ser Ser Leu Leu Gly Ser Leu Ser Asn Val Val Ser Val Thr
 20 25 30

Pro Cys Pro Tyr Leu Leu Ser Arg Tyr Lys Trp Ser Lys Gln Ile Leu
 35 40 45

Gly Phe His His Ser Glu Thr Asp Asn Cys Val Leu Asp Ile Leu Gln
 50 55 60

Lys Glu Gly Phe Gln Ser Lys Gly Ser His Tyr Phe Tyr Leu Thr His
 65 70 75 80

Lys Glu Ala Gly Asp Asn Trp Lys Val Pro Gly Glu Tyr Leu Gly Phe
 85 90 95

Gln Lys Ala Asp Met Ala Gln Cys Met His Ser Lys Ile Pro Leu Thr
 100 105 110

Phe Ile Glu Tyr Leu Leu Tyr Ala Cys Val Asn Ala Pro Cys Thr Leu
 115 120 125

Ser His Leu Arg Gly Trp Leu Trp Gly Arg Phe Tyr Pro Thr Phe Lys
 130 135 140

Gly Lys Val Glu Ile Val Thr Lys Trp Leu Arg Glu Asn Gly Gly Pro
 145 150 155 160

Ser Thr Ser Ser Arg Pro Gly Cys Pro His Cys Gly Leu Ser Gln Pro
 165 170 175
 Gly Ser Cys Gly Leu Tyr Arg Met Lys Pro Val Val Leu Val Thr Thr
 180 185 190
 Ser Ser Val Leu Ser Gln Pro Cys Leu Glu Gln Gly Val Arg Asp Ser
 195 200 205
 Leu Cys Phe Leu Asp Ser Asp Thr Leu Lys Gln Asn Gly Glu Cys Val
 210 215 220
 His Glu Gln Phe His Ser Gly Ser Met Val Asn Gly Gln Thr Asn Leu
 225 230 235 240
 Lys Arg Ser Ser Leu Trp Leu Glu Ser Pro Phe Ser Thr Pro Leu Ser
 245 250 255
 Ser Leu Pro Thr Phe Leu Ser Ser Trp Thr Phe Ile Ser Gly Lys Pro
 260 265 270
 Leu His Arg Cys Leu Cys Arg Ser Gln Ile Lys Asn Glu Arg Leu Ser
 275 280 285
 Pro Gly His Thr Lys Asn Leu Arg Arg Leu Phe Phe Gln Tyr Leu Lys
 290 295 300
 Asn Ser Cys Val Asp Asn Gly Arg Gly His Gln Arg Gln Asn Gln Lys
 305 310 315 320
 Gln Met Lys Arg Arg Pro Ser Phe Ser Gly Met Leu Leu Asn Gly Ala
 325 330 335
 Val Gly Gly Gln Ala Pro Leu Ser Leu Glu Ser Ala Leu Gln Gly Leu
 340 345 350
 His Ser Gly Ser Ser Gly Leu Arg Trp Arg Ala Leu Trp Lys Glu Phe
 355 360 365
 Leu Trp His Phe Arg Leu Trp Ile Ser Cys Glu Leu Glu Val Leu Arg
 370 375 380
 Pro His Asp Pro Ser Ile Glu Asp Lys Arg Val Gly Tyr Ile Cys Phe
 385 390 395 400
 Phe Leu Phe Leu Leu Phe Pro Arg Asn Arg Pro Ser Asn Cys Ser Gln
 405 410 415

85189-49001rev.txt

Ala Glu Ala Tyr Arg Asp Phe Phe Thr Leu Arg Arg Arg Thr Met Ile
420 425 430

Ser Gln Cys Ser Lys Trp Gly Lys Lys Arg Arg Glu Arg Glu Arg Glu
435 440 445

Arg Glu Arg Glu Arg Glu Arg Glu Arg Glu Arg Glu Arg Glu Arg Glu
450 455 460

Met Pro Arg Arg Ala Arg Gly Thr Lys Glu Val Gly Leu Cys Arg Gly
465 470 475 480

Gln Ile Ser Ile Glu Val Phe Ile Ser Ser Ala Leu Glu Asn Pro Ser
485 490 495

Ile Met Val Leu Val Thr Glu Ala Val Phe Thr Gly Lys Gln Asp Gln
500 505 510

Gly Ser Glu Gly Leu Pro Ile Thr Leu Ser Lys Gly Cys Val Ile Ala
515 520 525

Phe Glu Arg Thr Leu Ala Val Glu Arg Leu Leu Leu Pro Gln Ile Ile
530 535 540

Cys Leu Leu Arg Cys Ser Leu Arg Lys Ser Asp Cys Leu Pro Leu Leu
545 550 555 560

Gly Ala Trp Gly Lys Asp Leu Gly Lys Leu Arg Ala Asp Arg Arg Ser
565 570 575

Phe Ser Ala Leu His Ser Gln Ala Arg Glu Arg Gly Trp Gly Met Val
580 585 590

Gly Ala Asp Leu Cys Lys Gly Gly Trp His Cys Val
595 600

<210> 49
<211> 385
<212> PRT
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(385)
<223> J alpha DK1 sequence

<400> 49

Val Cys Leu Phe Leu Trp Ile Pro Asn Leu Ile His Cys Asp Lys Cys
Page 26

1 5 10 15

Lys Leu Phe Arg His Val Ser Gly Val Ser Thr Val Pro Ile His Pro
20 25 30

Asp Ile Thr Gly Ser Lys Val Pro Ser His Ala Phe Pro Val Leu Thr
35 40 45

Arg Lys Thr Gly Ser Ser Leu Tyr Cys Trp Gln Ala Gln Gly Ser Arg
50 55 60

Leu Glu Asp Ala Ser Asp Ala Gln Gln Pro Ala Trp Asp Cys Pro Gly
65 70 75 80

Arg Glu Ser Cys Ser Glu Met Pro Ser Ser Leu Pro Leu Gly Ile Ile
85 90 95

Leu Leu Ser Ser Pro Thr Ala Arg Pro Cys Leu Ser Val Ala Tyr Ser
100 105 110

Ile Pro Ala Ser His Thr Cys Gly Cys Ala Asn Ile Leu Ile Glu Ala
115 120 125

Ser Gly Arg Ser Gly Ser Ser Met Leu Leu Phe Gly Lys Ala Ser His
130 135 140

Ser Lys Ala Gly Leu Asp Ser Pro Pro Pro Lys Ser Leu His Ile Pro
145 150 155 160

Gly Ser Gly Leu Gln Val Gln Thr Thr Met Leu Val Phe Val Val Leu
165 170 175

Asp Met Glu Pro Gly Cys Ala Cys Leu Gln Gly Lys His Phe Ile Gly
180 185 190

Ala Ile Ser Leu Ala His Leu Pro Val Ser Ile Phe Phe Glu Arg Ile
195 200 205

Ser Trp Tyr Ser His Leu Val His Arg Gln Lys Asp Asp Val Asp Val
210 215 220

Pro Arg Trp His Thr Val Ile Trp Ser Gln Ala Leu Ile Phe Pro Pro
225 230 235 240

Ser Ile Phe Arg Cys Leu Ser Val Lys Val Ile Ser Ser Ser Met Ser
245 250 255

Pro Gly Gly Arg Leu Ala Cys Cys Pro Ser Ser Ala Val Ala Trp Met
 260 265 270

Ala Ser Ser Cys Tyr Pro Thr Leu Cys Ile Pro Ile Ile His Leu Thr
 275 280 285

Leu Tyr Val Tyr Leu Leu Phe Pro Tyr Ser Met Tyr Cys His Ala Thr
 290 295 300

Val Met Leu Phe Ile Val Ser Ser Val Ser Ser Val Val Pro Ile Thr
 305 310 315 320

Lys Ile Gln Arg Pro Asn Cys Leu Pro Cys Leu Lys Ile Ile Val Leu
 325 330 335

Glu Lys Lys Leu Glu Phe Cys Cys Cys Leu Tyr Arg His Glu Leu Arg
 340 345 350

Ser Leu Ala Val Ala Arg Thr Gly Tyr Asp Phe Cys Ser Val Leu His
 355 360 365

Thr Pro Val Met Arg Glu Pro Val Lys Asn Leu Gln Gly Leu Val Ser
 370 375 380

Leu
 385

<210> 50
 <211> 399
 <212> PRT
 <213> Mus musculus

<220>
 <221> misc_feature
 <222> (1)..(399)
 <223> J alpha TA39 sequence

<400> 50

Val Pro Asp Ser Trp Leu Arg Pro Pro Leu Ser His Ser Leu Tyr His
 1 5 10 15

Thr Asp Asp His Met Pro Tyr His Ser Ser Lys Val Glu Leu Gly Phe
 20 25 30

Asn Glu Glu Arg Asn Met Leu Leu Val Val Ala Val Leu His Pro Met
 35 40 45

Ser His Ser Met Phe Ile Ile Thr Leu Ile Thr Ser Ser Asp Lys Arg
 50 55 60

Lys Phe Thr Arg Arg Thr Val Thr Ile Cys Thr Leu Val Lys Met Lys
65 70 75 80

Val Ser Thr Gly Ala Gly Ala Tyr Cys Asn Ser Gly Tyr Gln Lys Asp
85 90 95

Gln Ala Leu Ala Arg Lys Lys Leu Asn Lys Val Asp Leu Val Lys Leu
100 105 110

Leu Gln Ile Phe Phe Lys Asn Gln Tyr Val Ser Glu Leu Thr Gly Glu
115 120 125

Tyr Ser Ala Ala Ile Leu Ser Gly Phe Ser Tyr Ser Tyr Gly Thr Thr
130 135 140

Val Val Glu Pro Cys Lys Arg Gly Phe His Gly Leu Asn Ser Met Leu
145 150 155 160

Ser Leu Tyr Ser Ser Asn Gln Lys Gly Gly Ile Pro Ser Arg Thr Pro
165 170 175

Lys Arg Glu Glu Ser Met Leu Ile Thr Ser Ile Asp His Ser Arg Leu
180 185 190

Ser Ile Phe Val Arg Gln His Gly Thr Thr Ile Tyr Asn Val Phe Ile
195 200 205

Trp Gly Thr Arg His His Arg Asp Ala Gly Cys Asp Pro Leu Asn Leu
210 215 220

Pro Gln Tyr Leu Gly Thr Val Val Lys Glu Leu Met Val His Ala Asp
225 230 235 240

Lys His Ile Pro Cys Met Gly Lys Leu Ser Lys Gly Cys Arg Thr Gly
245 250 255

Cys Glu Gln Asp Arg Ser Cys Arg Asn Pro Arg Asn Asn Ser Ser Arg
260 265 270

Arg Ala Asp Pro Glu Glu Arg Ala Ala Gln Leu Lys His Ile Gln Val
275 280 285

Pro Ile Cys Phe Asp Ser Cys Thr Gly Pro Ala Leu Ser Val Lys Arg
290 295 300

Lys Cys Leu Ile Ile Leu His Lys Leu Ile Gly Val Asn Val Cys Lys
Page 29

305

310

320

Asn Ile Leu Gln Ile Leu Lys Cys Tyr Pro His Ile Lys Tyr Gly Ser
325 330 335

Ile Lys Gln Gln Lys Ile Leu Lys Leu Gly Gln Ser Thr Leu Leu Arg
340 345 350

Arg Asp Gly Val Cys Ser Cys Gly Ser Val Ala Thr Gly Thr Gly Lys
355 360 365

His Pro Leu Ser Leu Met Glu Val Tyr Glu Leu Arg Val Thr Leu Met
370 375 380

Glu Thr Gly Arg Glu Arg Ser His Phe Val Lys Thr Ser Leu Thr
385 390 395

<210> 51
<211> 225
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(225)
<223> J beta 2.3 (bases 198551 to 198627), containing [SEQ ID NO:17]

<400> 51

Met Gly Leu Ser Ala Val Gly Arg Thr Arg Ala Glu Ser Gly Thr Ala
1 5 10 15

Glu Arg Ala Ala Pro Val Phe Val Leu Gly Leu Gln Ala Val Ser Thr
20 25 30

Asp Thr Gln Tyr Phe Gly Pro Gly Thr Arg Leu Thr Val Leu Glu Asp
35 40 45

Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser Glu
50 55 60

Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala Thr
65 70 75 80

Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly Lys
85 90 95

Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys Glu Gln
100 105 110

85189-49001rev.txt

Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg Val
115 120 125

Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln Val
130 135 140

Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg Ala
145 150 155 160

Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala Asp
165 170 175

Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr
180 185 190

Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu
195 200 205

Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp Ser Arg
210 215 220

Gly
225

<210> 52
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(39)
<223> J alpha 2 (bases 84269 to 84334)

<400> 52

Leu Leu Phe Lys Val Gly Pro Val Ser Leu Cys Asn Gly Val Thr Tyr
1 5 10 15

Gly Met Asn Thr Gly Gly Thr Ile Asp Lys Leu Thr Phe Gly Lys Gly
20 25 30

Thr His Val Phe Ile Ile Ser
35

<210> 53
<211> 142
<212> PRT
<213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(142)
 <223> J alpha 3 (83376. To 83437), containing [SEQ ID NO:18]

<400> 53

Leu Gln Gly Ile Glu Ala Ala Met Arg Glu Ala His Arg Pro Gly Glu
 1 5 10 15

Asn Leu Gly Ser Thr Leu Thr Gly Cys Phe Gln Ser Leu His Phe Leu
 20 25 30

Ser Ser Lys Met Thr Ile Thr Thr Ser Tyr Glu Ile Met Ala Arg Met
 35 40 45

Lys Val Ile Asn Lys Leu Phe Asn Ile Ile Ile Ile Ile Ile Ile Glu
 50 55 60

Ala Leu Leu Ile Leu Arg Phe Thr Leu Ser Arg Glu Arg Arg Ile Ala
 65 70 75 80

Ser Leu Gly Asn Lys Arg Cys Lys Gln Gln Arg Pro Lys Glu Pro Phe
 85 90 95

Arg Met Leu Leu Trp Asp Pro Ser Gly Phe Gln Gln Ile Ser Ile Lys
 100 105 110

Lys Val Ile Ser Lys Thr Leu Pro Thr Val Gly Val Gln Gln Cys Phe
 115 120 125

Gln Asp Asn Leu Trp Ile Arg Asp Gln Thr Gln His Pro Ala
 130 135 140

<210> 54
 <211> 162
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(162)
 <223> J alpha 6 (79270 to 79331), containing [SEQ ID NO:19], [SEQ ID NO
 :20], [SEQ ID NO: 21]

<400> 54

Gln Leu Gln Glu Lys Arg His Ile Lys Phe Pro Leu Leu Ser Val Leu
 1 5 10 15

Ala Ala Leu Ser Glu Ala Pro Cys Ile Leu Lys Ser Ser Arg Ala Arg
 Page 32

20

25

30

Pro Ser Glu Cys Leu Pro Gln Ala Ser Arg Val Trp Cys Leu Tyr Trp
 35 40 45

Gly Ala Gly Ser Arg His Gly Glu Leu Leu Pro Cys Phe Ser Ala Asp
 50 55 60

Gly Lys Val Val Phe Ser Pro Gly Tyr Thr Gly Ala Lys Glu Leu Ser
 65 70 75 80

Ser Pro Gln Pro Leu Ala Pro Ala Pro Gly Leu Gln His Ser Gly Ala
 85 90 95

Leu Arg Thr Ala Val Gly Asp Phe Leu Gln Leu Arg Glu Tyr Ser Gly
 100 105 110

Gly Phe Pro Arg Met Leu Pro Asn Thr Met Gly Gln Leu Val Glu Gly
 115 120 125

Gly His Met Lys Gln Val Leu Ser Lys Ala Val Leu Thr Val Cys Ile
 130 135 140

Arg Arg Lys Leu His Thr Tyr Ile Trp Lys Arg Asn Gln Pro Tyr Cys
 145 150 155 160

Ser Ser

<210> 55
 <211> 133
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(133)
 <223> J alpha 8 (76346 to 76405), containing [SEQ ID NO:22]

<400> 55

Ser Ile His Gly His His Ser Cys Lys Lys His Val Leu Thr Asn Ser
 1 5 10 15

Val Trp Met Val Lys Leu Pro Val Leu Ser Arg Thr Glu Thr Leu Leu
 20 25 30

Tyr Leu Phe Leu Glu Tyr His Phe Tyr Ile Thr Gln Gly Ile Gln Ser
 35 40 45

85189-49001rev.txt

Arg Ile Phe Ser Trp Val Leu Ser Asp Leu Leu Ser Ser Ser Asn Gly
50 55 60

Leu Arg Lys Ile Lys Val Lys Asp Met Pro Pro Thr Thr Leu Val His
65 70 75 80

Ala Cys Arg His Arg Asn Thr Leu Ser Asn Leu Ala Cys Asp Leu Ala
85 90 95

Ile Leu Ala Met Ala Gln Gln Gly Pro Ile Leu Tyr Arg Val Met Ser
100 105 110

Glu Cys Glu His Arg Leu Ser Glu Thr Cys Ile Trp Asn Trp His Pro
115 120 125

Thr Ser Gly Gln Ser
130

<210> 56
<211> 158
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(158)
<223> J alpha 9 (75756 to 75816), containing [SEQ ID NO:23]

<400> 56

Gln Tyr Asn Ser Thr Arg Ala Leu Leu Cys Glu Leu Arg Asn Ala Gly
1 5 10 15

Arg His Phe Ala His Arg Thr Leu Ala Leu Arg Asp Ser Leu Lys Ile
20 25 30

Ser Ser Ser Pro Leu Phe Ile Phe Pro Ile Arg Lys Leu Arg Pro Arg
35 40 45

Glu Val Gly Ile Val Gly Gln Cys Glu Leu Gly Leu Gly Leu Glu Pro
50 55 60

Gly Asp Pro Gly Pro Gly Ala Ile Phe Cys Asp Cys Cys Leu Val Asn
65 70 75 80

Thr Ser Asp Arg Glu Val Val Met Leu Ile Asn Arg Lys Asn Lys Val
85 90 95

Leu Gln Gly Glu Tyr Lys Asn Val Leu Leu Ile Thr Ser Thr Leu Val
Page 34

100

105

110

Ala Pro Thr Cys Ser Pro Ala Val Val Lys Trp Lys Glu Lys Glu Met
 115 120 125

Ala His Phe Val Ala Val Gln Ile Thr Val Gly Asn Thr Gly Gly Phe
 130 135 140

Lys Thr Ile Phe Gly Ala Gly Thr Arg Leu Phe Val Lys Ala
 145 150 155

<210> 57
 <211> 168
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(168)
 <223> J alpha 11(72705 to 72765), containing [SEQ ID NO:24]

<400> 57

Val Asn Ser Gly Tyr Ser Thr Leu Thr Phe Gly Lys Gly Thr Met Leu
 1 5 10 15

Leu Val Ser Pro Glu His Cys Tyr Ser Ser Asp Val Trp Phe Gln Lys
 20 25 30

Asn Pro Asn Ile Ala Val Ile Pro Leu Lys Glu Gln Gly Arg Gly Phe
 35 40 45

Phe Ser Glu Ser Ser Ser Asp Leu Ser Ile Leu Cys Gln Ser Val Leu
 50 55 60

Trp Ile Gln Asp Thr Tyr Ile Phe Val Ser Ser Ala Gly Pro Thr Cys
 65 70 75 80

Ser Ala Ser Asp His Leu Ser Leu Ile Cys Lys Met Arg Ile Ile Phe
 85 90 95

Lys Leu Met Ala Gln Leu Lys Pro Lys Gly Ser Gly Ile Tyr Ala Asp
 100 105 110

Tyr Ser Ile Trp Leu Ile Asn Glu Gly Phe Leu Ser Phe Ser Leu Cys
 115 120 125

Arg Ser Trp Val Glu Ile Pro Asn Thr Ala Asn His Phe Cys Met Gly
 130 135 140

Ile Cys Tyr Ser Val Asn Ser Gly Tyr Ser Thr Leu Thr Phe Gly Lys
 145 150 155 160

Gly Thr Met Leu Leu Val Ser Pro
 165

<210> 58
 <211> 170
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(170)
 <223> J alpha 13 (71282 to 71342), containing [SEQ ID NO:25]

<400> 58

Asp Lys Ile Leu Glu Ser Ser Arg Lys Arg Gln Lys Val Trp Leu Ser
 1 5 10 15

Thr Ser Ser Ser Ser Asp Leu Ala Leu Val Asn Leu Gly His Ser Ile
 20 25 30

Phe Ile Tyr Lys Met Lys Thr Phe Asn Ile Thr Ser Asp Phe Leu Phe
 35 40 45

Phe Cys Gly Tyr Ile Ile Gly Val Tyr Ile Tyr Phe Lys Asp Lys Leu
 50 55 60

Ile Tyr Val Lys Val Phe Cys Lys Phe Leu Asn Ala Ile His Ser Glu
 65 70 75 80

Asn Ile Ile Cys Leu Asn Lys Lys Asn Tyr Val Arg Phe Arg Ile Leu
 85 90 95

Leu Thr Glu Phe Val Gly Ser Asn Ser His Leu His Val Ile Cys Ser
 100 105 110

Pro Arg His Trp Lys Ala Leu Ser Leu Leu Leu Lys Tyr Ser Gly Ser
 115 120 125

Asn Ala Thr Gln Met Lys Arg Ala Gly Glu Gly Lys Ser Phe Cys Lys
 130 135 140

Gly Arg His Tyr Ser Val Asn Ser Gly Gly Tyr Gln Lys Val Thr Phe
 145 150 155 160

Gly Ile Gly Thr Lys Leu Gln Val Ile Pro

165

<210> 59
<211> 163
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(163)
<223> J alpha 14 (70532 to 70583), containing [SEQ ID NO:26]

<400> 59

Ser Tyr Ser Met Leu Leu Lys Lys Phe Leu Ile Glu Glu Arg Lys Ile
1 5 10 15

Ile Tyr Lys Asp Met Ser Asn Leu Leu Asn Ser Gly Lys Met Arg Leu
20 25 30

Cys Thr Gly Val Asp Ser Val Lys Met Gly Val Arg Ala Ala Ile Leu
35 40 45

Trp Leu Val Lys Gln Asp Tyr Leu Val Lys Leu Cys Lys Ser Pro Arg
50 55 60

Lys Lys Val Ser Glu Leu Ser Arg Glu Tyr His Leu Asp Cys Ser Gln
65 70 75 80

Ala Phe His Tyr Ile Tyr Cys Thr Thr Met Val Pro Lys Glu Ala Phe
85 90 95

Ser Gly Leu Ile Pro Trp Leu Ser Leu Tyr Ser Ser Ile Lys Lys Gly
100 105 110

Glu Ser Ser Gln Ser Ser His Glu Gly Asp Ser Cys Met Leu Thr Thr
115 120 125

Leu Ile Tyr Tyr Gln Gly Asn Ser Val Ile Phe Val Arg Gln His Ser
130 135 140

Ala Val Ile Tyr Ser Thr Phe Ile Phe Gly Ser Gly Thr Arg Leu Ser
145 150 155 160

Val Lys Pro

<210> 60
<211> 142
<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(142)

<223> J alpha 24 (60203 to 60265), containing [SEQ ID NO:27]

<400> 60

Lys Thr Ser Ser Tyr Leu Asn Asp Arg Ala Thr Val Val Ile Ser Cys
1 5 10 15

His Leu Ser Ser Ala Glu Asp Trp Val Pro Val Asn Ala Ala Gly Gly
20 25 30

Phe Leu Ser Leu Gln His Leu Lys Arg Thr Pro Arg Leu His Pro Gln
35 40 45

Gln Ser Gly Phe Leu Pro Leu Pro Pro Gly Arg Cys Ser Ser Trp His
50 55 60

Thr Pro Ser Leu Val Ser Lys Lys Arg Asn Lys Arg Lys Gly Glu Lys
65 70 75 80

Leu Ile Ser His Ile Met Gln Leu Pro His Phe Val Ala Arg Leu Phe
85 90 95

Pro His Glu Gln Phe Val Phe Ile Gln Gln Leu Ser Ser Leu Gly Lys
100 105 110

Pro Phe Cys Arg Gly Val Cys His Ser Val Thr Thr Asp Ser Trp Gly
115 120 125

Lys Leu Gln Phe Gly Ala Gly Thr Gln Val Val Val Thr Pro
130 135 140

<210> 61

<211> 176

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(176)

<223> J alpha 25 (59046 to 59105)

<400> 61

Gln Lys Asp Lys Ala Ser Pro Leu Ser Leu Gly Arg Gly Gln Gly Cys
1 5 10 15

Leu Ser Ser Gln Ala Gln Ala Gly Gly Arg Lys Leu Gly Val Phe Ala
 20 25 30

Glu Pro Arg Asn Thr Val Gly Ile Thr Met Val Arg Ile Leu Ser Leu
 35 40 45

Val Pro Glu Pro Asp Cys Pro Cys Cys Pro Val Ser Thr Val Lys Trp
 50 55 60

Arg Lys Met Ser Pro Val Leu Asp Val Gly Arg Ser Cys Arg Val Leu
 65 70 75 80

Arg Pro Gly Val His Arg Asp Leu Arg Ser Gly Asp Gly Glu Glu Gly
 85 90 95

Lys Arg Asn Glu Lys Gln Asn His Lys Asp Asn Thr Glu Glu Gly Phe
 100 105 110

Ile Phe Gly Lys Glu Asn His Lys Ala Val Leu Thr Leu Glu Glu Met
 115 120 125

His Ser Phe Gly Gly Ser Leu Leu Arg Arg Ala Leu Cys Arg Gly Lys
 130 135 140

Leu Ser Cys Val Phe Asp Ala Glu Ile Ile Thr Met Gln Lys Asp Lys
 145 150 155 160

Ala Ser Pro Leu Ser Leu Gly Arg Gly Gln Gly Cys Leu Ser Ser Gln
 165 170 175

<210> 62
 <211> 141
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(141)
 <223> J alpha 31 (51207 to 51263), containing [SEQ ID NO:28]

<400> 62

Glu Leu Gly Trp Leu Cys Ser Trp Lys Ile Ser Leu Trp Val Glu Cys
 1 5 10 15

Thr Val Pro Ser Asn Leu Cys Val Gly Ala His Thr Tyr Asp Ser Lys
 20 25 30

Ser Cys Gln Ile Arg Phe Ser Phe Gly Ser Phe Met Pro Arg Asn Ala
 35 40 45

85189-49001rev.txt

Lys Glu Phe Lys Leu Ile Ser Leu Ala Phe Leu Lys Glu Thr Leu Phe
50 55 60

Ala Leu Cys Cys Arg Ala Asn Phe Ser Ser Tyr His Lys Arg Pro Glu
65 70 75 80

Thr Gln Arg Lys Gln Lys Lys Lys Arg Lys Lys Lys Lys Thr Gln Gly
85 90 95

Glu Ser Asn Cys Pro Leu Thr Thr Val Leu Cys Val Trp Gly Phe Thr
100 105 110

Met Gly Phe Ser Lys Gly Arg Lys Cys Cys Gly Asn Asn Ala Arg
115 120 125

Leu Met Phe Gly Asp Gly Thr Gln Leu Val Val Lys Pro
130 135 140

<210> 63
<211> 148
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(148)
<223> J alpha 36 (45351 to 45411), containing [SEQ ID NO:29]

<400> 63

Lys Leu Gly Ala Val Ser Leu Thr Cys Asn Leu Ser Ile Leu Glu Gly
1 5 10 15

Gly Arg Arg Ile Thr Gly Gln Glu Phe Lys Thr Thr Leu Gly Asn Thr
20 25 30

Val Arg Pro Pro Ser Leu Gln Lys Ile Asn Lys Asn Phe Phe Lys Asn
35 40 45

Ser Gln Ala Trp His Ala Pro Val Ile Leu Ala Thr Glu Glu Val Glu
50 55 60

Ala Gly Gly Ser Leu Val Pro Arg Arg Ser Arg Leu Gln Ala Lys Asn
65 70 75 80

Thr Pro Leu His Ser Ser Leu Asp Asn Lys Val Arg Ser Cys Leu Lys
85 90 95

Tyr Ile Phe Lys Asn Ile Lys Ile Ser Arg Arg Arg Lys Glu Met Lys
 100 105 110

Lys Ile Trp Leu Ser Arg Lys Val Phe Leu Tyr Trp Ala Glu Thr Leu
 115 120 125

Cys Gln Thr Gly Ala Asn Asn Leu Phe Phe Gly Thr Gly Thr Arg Leu
 130 135 140

Thr Val Ile Pro
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<210> 64
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 <222> (1)..(144)
 <223> J alpha 40 (39930 to 39990), containing [SEQ ID NO:30], [SEQ ID N
 O:31], [SEQ ID NO:32], [SEQ ID NO:33]

<400> 64

Asn Tyr Lys Ile Met Ser Trp Val Cys Leu Cys Gly Ser Thr Gly Ser
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Arg Gly Glu Ser Met Glu Tyr Phe Arg Gly Phe Asn Ser His Leu Asp
 20 25 30

Ala Val Leu Ile Cys Ser Leu Asn Gln Thr Leu Leu Ile Asn Met His
 35 40 45

Lys Asp Ser Met Arg Leu Lys Asn Phe Cys Lys Leu Gly Pro Asn Arg
 50 55 60

Ser Ser Glu Asp Phe Leu Tyr Glu Leu Arg Tyr Asn Pro Lys Ile Thr
 65 70 75 80

Cys Arg Lys Ile Arg Gly Gln Gly Leu Ser Met Gly Lys Val His Val
 85 90 95

Met Pro Leu Leu Phe Met Glu Ser Lys Ala Ala Ser Ile Asn Gly Asn
 100 105 110

Ile Met Leu Val Tyr Val Glu Thr His Asn Thr Val Thr Thr Ser Gly
 115 120 125

Thr Tyr Lys Tyr Ile Phe Gly Thr Gly Thr Arg Leu Lys Val Leu Ala
 Page 41

130

135

<210> 65
<211> 152
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(152)
<223> J alpha 41 (37899 to 37961), containing [SEQ ID NO:34], [SEQ ID N
0:35]

<400> 65

Gln Leu Leu Ser Leu Tyr Leu Pro Pro Thr Phe Thr Leu Glu Pro His
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Arg Ile Val Ser Val His Ala Pro Gly Cys Ser Gln Ser Arg Pro Ala
20 25 30

Arg Arg Ser Ala Gly His Arg Lys Thr Pro Asp Phe Ile Thr Cys His
35 40 45

Arg Ala Pro Ser Leu Arg Trp Gln Ile Ser Ile Leu Ile Thr His Ile
50 55 60

Thr Val Gly Ser Gly Asp Leu Val Ser Asn Gly Leu Met Glu Glu Gly
65 70 75 80

Ser Phe Ile Tyr Thr Ile Lys Gly Pro Trp Met Thr His Ser Leu Cys
85 90 95

Asp Cys Cys Val Ile Gly Phe Gln Thr Leu Ala Leu Ile Gly Ile Ile
100 105 110

Gly Glu Gly Thr Trp Trp Leu Leu Gln Gly Val Phe Cys Leu Gly Arg
115 120 125

Thr His Cys Gly Thr Gln Ile Pro Gly Met His Ser Thr Ser Ala Lys
130 135 140

Ala Pro Arg Cys Trp Ser His Pro
145 150

<210> 66
<211> 141
<212> PRT
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<220>

<221> misc_feature
 <222> (1)..(141)
 <223> J alpha 44 (35064 to 35126), containing [SEQ ID NO:36]

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Leu Gly Pro Ile Thr His Gln Val Gln Glu Gly Phe Ile Lys Ile Lys
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Pro Arg Asn Arg Lys Asp Lys Glu Phe Asn Ser Gln Cys Leu Gln Ser
 20 25 30

Thr Gln Leu Leu Ser Leu Asn His Leu Val Ser Thr Pro Pro Thr Glu
 35 40 45

Val Lys Glu Gly Asn Gln Gln Val Met Leu Val Lys Val Ser Gly Gln
 50 55 60

Ser Gln Leu Pro Ser Glu Leu Ile Leu Trp Ser Leu Gly Lys Gly Asn
 65 70 75 80

Ala Ser Val Arg Ala His Pro Gly Cys Pro Ser Gly Arg Asp His Gly
 85 90 95

Glu Ser Ser Glu Gly Ser Glu His Gln Met Glu Ser Gln Ala Thr Gly
 100 105 110

Phe Cys Tyr Glu Ala Ser His Ser Val Asn Thr Gly Thr Ala Ser Lys
 115 120 125

Leu Thr Phe Gly Thr Gly Thr Arg Leu Gln Val Thr Leu
 130 135 140

<210> 67
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 <223> intron 5 prime to J beta 2.3

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 <222> (93)..(138)
 <223> J beta 2.3 sequence

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<223> C beta 2 domain

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tccgagtcct accagcaagg ggtcctgtct gccaccatcc tctatgagat cttgctaggg    600
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Asp Thr Gln Tyr Phe Gly Pro Gly Thr Arg Leu Thr Val Leu Glu Asp
35          40          45

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Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser Glu
50          55          60

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Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala Thr
65          70          75          80

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Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly Lys
85          90          95

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Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys Glu Gln
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85189-49001rev.txt

Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg Val
 115 120 125

Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln Val
 130 135 140

Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg Ala
 145 150 155 160

Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala Asp
 165 170 175

Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr
 180 185 190

Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu
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<400> 86

Met Met Leu Val
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85189-49001rev.txt